to extracellular domains (ECD), transmembrane domains (TM) and cytoplasmic domains (CD); (c) nucleotides that encode mutants of a differentially expressed and/or pathway gene, product, in which all or part of one of its domains is

5   deleted or altered, and which, in the case of receptor-type gene products, such mutants include, but are not limited to, soluble receptors in which all or a portion of the TM is deleted, and nonfunctional receptors in which all or a portion of CD is deleted; and (d) nucleotides that encode

10 fusion proteins containing a differentially expressed and/or pathway gene product or one of its domains fused to another polypeptide.

The nucleotide sequences of the invention further include nucleotide sequences corresponding to the nucleotide

15 sequences of (a)-(d) above wherein one or more of the exons, or fragments thereof, have been deleted.

The nucleotide sequences of the invention still further include nucleotide sequences that have at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or more nucleotide sequence

20 identitiy to the nucleotide sequences of (a)-(d) above. The nucleotide sequences of the invention also include nucleotide sequences that encode polypeptides having at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or higher amino acid sequence identity to the polypeptides encoded by the nucleotide

25 sequences of (a)-(d) above.

To determine the percent identity of two amino acid sequences or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic

30 acid sequence for optimal alignment with a second amino aor nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue

35 or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function

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of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical overlapping positions/total # of positions x 100%). In one embodiment, the two sequences are the same length.

5   The determination of percent identity between two sequences can also be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990)

10 *Proc. Natl. Acad. Sci. U.S.A.* *87*:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. U.S.A.* *90*:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.*, 1990, *J. Mol. Biol.* *215*:403-0. BLAST nucleotide searches can be performed

15 with the NBLAST nucleotide program parameters set, *e.g.*, for score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the present invention. BLAST protein searches can be performed with the XBLAST program parameters set, *e.g.*, to score-50,

20 wordlength=3 to obtain amino acid sequences homologous to a protein molecule of the present invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, 1997, *Nucleic Acids Res.* *25*:3389-3402. Alternatively, PSI-BLAST can be used to

25 perform an iterated search which detects distant relationships between molecules (*Id.*). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, of XBLAST and NBLAST) can be used (see, *e.g.*, http://www.ncbi.nlm.nih.gov). Another

30 preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) *CABIOS* *4*:11-17. Such an algorithm is incorporated in the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When

35 utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

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The percent identity between two sequences can be
determined using techniques similar to those described above,
with or without allowing gaps. In calculating percent
identity, typically only exact matches are counted.

5   The invention also includes nucleic acid molecules,
preferably DNA molecules, that hybridize to, and are
therefore the complements of, the DNA sequences (a) through
(d), in the preceding paragraph. Such hybridization
conditions can be highly stringent or less highly stringent,

10 as described above. The nucleic acid molecules of the
invention that hybridize to the above described DNA sequences
include oligodeoxyoligonucleotides ("oligos") which hybridize
under highly stringent or stringent conditions to the DNA
sequences (a) through (d) in the preceding paragraph. In

15 general, for oligos between 14 and 70 nucleotides in length
the melting temperature (Tm) is calculated using the formula:
$Tm(°C) = 81.5 + 16.6(\log[\text{monovalent cations (molar)}] + 0.41$
$(\% \ G+C) - (500/N)$, where N is the length of the probe. If
the hybridization is carried out in a solution containing

20 formamide, the melting temperature may be calculated using
the equation: $Tm(°C) = 81.5 + 16.6(\log[\text{monovalent cations}$
$(\text{molar})]) + 0.41(\% \ G+C) - (0.61\% \ \text{formamide}) - (500/N)$ where N
is the length of the probe. In general, hybridization is
carried out at about 20-25 degrees below Tm (for DNA-DNA

25 hybrids) or about 10-15 degrees below Tm (for RNA-DNA
hybrids). Other examplary highly stringent conditions may
refer, e.g., to washing in 6xSSC/0.05% sodium pyrophosphate
at 37°C (for 14-base oligos), 48°C (for 17-base oligos), 55°C
(for 20-base oligos), and 60°C (for 23-base oligos).

30   These nucleic acid molecules can encode or act as target
gene antisense molecules, useful, for example, in target gene
regulation and/or as antisense primers in amplification
reactions of target, fingerprint, and/or pathway gene nucleic
acid sequences. Further, such sequences can be used as part

35 of ribozyme and/or triple helix sequences, also useful for
target gene regulation. Still further, such molecules can be
used as components of diagnostic methods whereby the presence

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